



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 137505

TO: Patricia Duffy
Location: REM/3B05/3C18
Art Unit: 1645
Monday, November 15, 2004
Case Serial Number: 09/765271

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: (571)272-2527

paul.schulwitz@uspto.gov

Search Notes

Examiner Duffy,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2527

Allice

STIC-Biotech/ChemLib

757505

From: Duffy, Patricia
Sent: Tuesday, November 09, 2004 3:48 PM
To: STIC-Biotech/ChemLib
Subject: Quick comparison search of proteins.

Importance: High

IN re:09/765,271

Please run a comparison sequence search comparing SEQ ID NO:56 of 09/765,271 with Accession Number P91742 of SPTREMBL. I need the full length of p19742 compared. I am looking for a short region that has 8 consecutive amino acids in common with SEQ ID NO:56.

Thank you.

Patricia A. Duffy, Ph.D.
Art Unit 1645, Remsen 3B05
571-272-0855

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: 11/15
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: November 15, 2004, 16:56:34 ; Search time 0.001 Seconds
(without alignments)
122.584 Million cell updates/sec

Title: us-09-765-271-56
Perfect score: 4165
Sequence: 1 SYELGLYQARTVKNRVSY.....KLLALLKGSNPSSVSKKIN 796

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 154 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : p91742.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52.5	1.3	154	1 p91742	TOIG of: p91742

ALIGNMENTS

RESULT 1
p91742
; TOIG of: p91742 check: 1859 from: 1 to: 154
; ID p91742 PRELIMINARY; PRT; 154 AA.
; AC p91742;
; DT 01-MAY-1997 (TrEMBLrel. 03, Created)
; DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
; DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
; DE Transposase (Fragment).
; OS Hydra attenuata (Hydra) (Hydra vulgaris).
; OC Eukaryota; Metazoa; Chnidaria; Hydrozoa; Hydroida; Anthomedusae;
; OC Hydridae; Hydra.
; OX NCBI_TaxID=6087;
; RN [1]
; RP SEQUENCE FROM N.A.
; RC TRANSPOSOMARINER;
; RX MEDLINE=97327060; PubMed=9183847;
; RA Robertson H.M.;
; RT "Multiple Mariner transposons in flatworms and hydras are related to
; RT those of insects.";
; RL J. Hered. 88:195-201(1997).
; DR EMBL; U51185; AAB61389.1; -.
; DR InterPro; IPR001888; Transposase 1.
; DR Pfam; PF01359; Transposase_1; 1.
; FT NON_TER 1
; FT NON_TER 154 154